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FIG 12

## Anti-KIR light variable regions

1 50  
 DF-200 light variable (1) M--ESQTLVFLSILLWLYGADGNIVMTQSPKSMSSMSGGERVLTCKASEN  
 PAN2D-Light-variable (1) MDFQVQIFSFLISASVIMSRGQIVLTQSPASMSASGGERVLTCTASSS  
 Consensus (1) Q F I I L A G N I V L T Q S P S M S S L G E R V L T L C A S  
 100  
 DF-200 light variable (49) VVTRNWSYQQKPEQSPKLLIYGASNRYLGVPDRFTGSGSADFTLTSS  
 PAN2D-Light-variable (51) VSSSYLVWYQQKPGSSPKLWIYSTNLA\$GVPA\$FSGSG\$CT\$SLTSS  
 Consensus (51) V S Y L W Y Q Q K P S P K L I Y S N S G V P R F S G S G S A T F S L T I S S  
 101 131  
 DF-200 light variable (98) VQAEADIAVTCGQGSYPYTFGGGKLEIKR (SEQ ID NO:1)  
 PAN2D-Light-variable (101) VEAEDAAVYCHQYERSPPTFEGGKLEIKR (SEQ ID NO:2)  
 Consensus (101) M A E D A Y H C Q H P T F G G G T K L E I K R (SEQ ID NO:13)

Numbers above amino acid sequences indicate position respective to initiation of translation Met (+1) in the immature (non-secreted) immunoglobulin. Underlined are the CDR regions

## CDR's from the anti-KIR light variable regions

CDR-L1 from clones PAN-2D and DF-200	
Residue before: Normally Cys. Residues after: Trp. Typically Trp-Tyr-Leu. Length: 10-17 aa	CDR -L2 from clones PAN-2D and DF-200 Residues before: Generally Ile-Tyr Length: 7 aa Start: approximately 16 aa after the end of CDR-L1
DF-200 light variable (44) KASEN <u>VV</u> LT- <u>Y</u> VS (SEQ ID NO:3) PAN2D-Light-variable (46) TASSSVSS <u>SY</u> LY (SEQ ID NO:4) Consensus AS V S YL (SEQ ID NO:14)	DF-200 light variable (70) GASNRY <u>Y</u> (SEQ ID NO:5) PAN2D-Light-variable (73) STSNLA <u>S</u> (SEQ ID NO:6) Consensus SN S (SEQ ID NO:15)
CDR-L3 from clones PAN-2D and DF-200	
Residues before: Cys Residues after: Phe-Gly-XXX-Gly Length: 7-11 aa Start: approximately 33 aa after the end of CDR-L2	
DF-200 light variable (109) GQG <u>SY</u> PYT (SEQ ID NO:7) PAN2D-Light-variable (112) HQY <u>RS</u> PEPT (SEQ ID NO:8) Consensus Q H P T (SEQ ID NO:16)	

FIG 13

>DF-200\VH\immature-PROT  
MAVLGLLFLCLVTFPSCVLS  
QVQLEQSGPGLVQPSQSL SITCTVSGFSFTPYGVHVVRRQSPGKGLEWLGVWSSGGNTDYNAAFISRLSINKDNSKSQVFFK  
MNSLQVNDTAIYYCARNPRPGNYPYGM DYWGQGTSTVTSS (SEQ ID NO: 9)

Anti-KIR heavy variable regions (immature Fabs)

Sequences including CDR regions in heavy variable regions

<b>CDR-H1 from clone DF-200</b> Residues before: Cys-XXX-XXX-XXX Residues after: Trp. Generally Trp-Val or Trp-Ile Length: 10-14 aa Start: Approximately 22-26 aa from the beginning of the secreted protein  GFSFTPYGVH (SEQ ID NO: 10)	<b>CDR-H2 from clone DF-200</b> Residues before: Leu-Glu-Trp-Ile-Gly but other variations possible Residues after: Lys or Arg / Leu or Ile or Val or Phe or Thr or Ala / Thr or Ser or Ile or Ala Length: 16-20 aa Start: Approximately 15 aa after the end of CDR-H1  VIWSSGGNTDYNAAFIS (SEQ ID NO: 11)
<b>CDR-H3 from clones 4G1, 5D5 and 6C12</b> Residues before: Cys-XXX-XXX (Typically Cys-Ala-Arg) Residues after: Trp-Gly-XXX-Gly Length: 3-25 aa Start: Approximately 33 after the end of CDR-H2  NPRPGNYPYGM DY (SEQ ID NO: 12)	

The secreted, mature VH starts at:  
Position 20: residue Q

The VH region ends with residue S and thereafter the constant region (not shown ) continues